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(54) Title: CANCER ASSOCIATED GENES AND THEIR PRODUCTS

(57) Abstract: The application discloses cancer-associated genes and their products, especially those identifiable by SEREX. The genes and products are used to identify, track and treat cancer. Preferably the cancer is prostate cancer.

CANCER ASSOCIATED GENES AND THEIR PRODUCTS.

The invention relates to isolated nucleic acid sequences which are expressed in cancers, especially prostate cancers, to their protein products and to the use of the nucleic acid and protein products for the identification and treatment of prostate cancers.

The prostate gland is an accessory sex gland in males which is wrapped around the urethra as this tube leaves the bladder. The gland secretes an alkaline fluid during ejaculation. Cancer of the prostate gland is very serious and represents the second leading cause of death from cancer in men.

Two specific proteins are known to be made in very high concentrations in prostate cancer cells. These are prostatic acid phosphatase (PAP) and prostate specific antigen (PSA). These proteins have been characterised and have been used to follow response to therapy. However, it has been difficult to correlate the presence of these two proteins to the presence of cancer.

Accordingly, there is a need to identify new genes and proteins which are associated with the presence of prostate cancer.

The inventors have used a technique known as SEREX (Serological Identification of Antigens by Recombinant Expression Cloning) to identify genes which are over-expressed in prostate cancer tissue. This technique was published by Sahin *et al* (PNAS (USA), 1995, Vol. 92, pages 11810-11813). SEREX uses total RNA isolated from tumour

biopsies from which poly(A)$^+$ RNA is then isolated. cDNA is then produced using an oligo (dT) primer. The cDNA fragments produced are then cloned into a suitable expression vector, such as a bacteriophage and cloned into a suitable host, such as E.coli. The clones produced are screened with high-titer IgG antibodies in autologous patient serum, to identify antigens associated with the tumour.

The inventors have used this technique to identify a number of genes and gene products associated with prostate cancer. Furthermore, preliminary results have found that some antigens identified by this technique have been also identified by the inventors as being associated with other cancers, such as stomach cancer and oesophagial cancer.

A first aspect of the invention provides an isolated mammalian nucleic acid molecule selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66. Preferably the isolated nucleic acid molecule encodes a mammalian antigen which is expressed in higher than normal concentrations in cancer cells, compared with normal non-cancerous cells. Preferably the cancer is prostate

cancer. The term "higher than normal concentrations" preferably means that the protein is expressed at a concentration at least 5 times greater in tumour cells than normal cells.

The invention also includes, within its scope, nucleic acid molecules complementary to such isolated mammalian nucleic acid molecules.

The nucleic acid molecules of the invention may be DNA, cDNA or RNA. In RNA molecules "T" (Thymine) residues may be replaced by "U" (Uridine) residues.

Preferably, the isolated mammalian nucleic acid molecule is an isolated human nucleic acid molecule.

The invention further provides nucleic acid molecules comprising at least 15 nucleotides capable of specifically hybridising to a sequence included within the sequence of a nucleic acid molecule according to the first aspect of the invention. The hybridising nucleic acid molecule may either be DNA or RNA. Preferably the molecule is at least 90% homologous to the nucleic acid molecule according to the first aspect of the invention. This may be determined by techniques known in the art.

The term "specifically hybridising" is intended to mean that the nucleic acid molecule can hybridise to nucleic acid molecules according to the invention under conditions of high stringency. Typical conditions for high stringency include 0.1 x SET, 0.1% SDS at 68°C for 20 minutes.

The invention also encompasses variant DNAs and cDNAs which differ from the sequences identified above, but encode the same amino acid sequences as the isolated mammalian nucleic acid molecules, by virtue of redundancy in the genetic code.

	U		C		A		G		
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA*	Stop	UGA*	Stop	A
	UUG		UCG		UAG*	Stop	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	Lys	AGA	Arg	A
	AUG**	Met	ACG		AAG		AGG		G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	Glu	GGA		A
	GUG**		GCG		GAG		GGG		G

* Chain-terminating, or "nonsense" codons.

** Also used to specify the initiator formyl-Met-tRNAMet. The Val triplet GUG is therefore "ambiguous" in that it codes both valine and methionine.

The genetic code showing mRNA triplets and the amino acids which they code for.

The invention also includes within its scope vectors comprising a nucleic acid according to the invention. Such vectors include bacteriophages, phagemids, cosmids and plasmids. Preferably the vectors comprise suitable regulatory sequences, such as promoters and termination sequences which enable the nucleic acid to be expressed upon insertion into a suitable host. Accordingly, the invention also includes hosts comprising such a vector. Preferably the host is E.coli.

A second aspect of the invention provides an isolated protein or peptide obtainable from a nucleic acid sequence according to the invention. As indicated above, the genetic code for translating a nucleic acid sequence into an amino acid sequence is well known.

The invention further provides polypeptide analogues, fragments or derivatives of antigenic polypeptides which differ from naturally-occurring forms in terms of the identity of location of one or more amino acid residues (deletion analogues containing less than all of the residues specified for the protein, substitution analogues wherein one or more residues specified are replaced by other residues in addition analogues wherein one or more amino acid residues are added to a terminal or medial portion of the polypeptides) and which share some or all properties of the naturally-occurring forms. Preferably such polypeptides comprise between 1 and 20, preferably 1 and 10 amino acid deletions or substitutions.

Preferably the protein or peptide is at least 95%, 96%, 97%, 98% or 99% identical to the sequences of the invention. This can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive,

Madison, WI 53711). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The nucleic acids and proteins/peptides of the invention are preferably identifiable using the SEREX method. However, alternative methods, known in the art, may be used to identify nucleic acids and protein/peptides of the invention. These include differential display PCR (DD-PCR), representational difference analysis (RDA) and suppression subtracted hybridisation (SSH).

All of the nucleic acid molecules according to the invention and the peptides which they encode are detectable by SEREX (discussed below). The technique uses serum antibodies from prostate cancer patients to identify the molecules. It is therefore the case that the gene products identified by SEREX are able to evoke an immune response in a patient and may be considered as antigens suitable for potentiating further immune reactivity if used as a vaccine.

The third aspect of the invention provides the use of nucleic acids or protein/peptides according to the invention, to detect or monitor prostate cancer.

The use of a nucleic acid molecule hybridisable under high stringency conditions, a nucleic acid according to the first aspect of the invention to detect or monitor prostate cancer is also encompassed. Such molecules may be used as probes, e.g. using PCR.

The expression of genes, and detection of their protein products and/or peptides may be used to monitor disease progression during therapy or as a prognostic indicator of the initial disease status of the patient. There are a number of techniques which may be used to detect the presence of a gene, including the use of Northern blot and reverse transcription polymerase chain reaction (RT-PCR) which may be used on tissue or whole blood samples to detect the presence of cancer associated genes. For protein and/or peptide sequences in-situ staining techniques or enzyme linked ELISA assays or radio-immune assays may be used. RT-PCR based techniques would result in the amplification of messenger RNA of the gene of interest (Sambrook, Fritsch and Maniatis, Molecular Cloning, A Laboratory Manual, 2nd Edition). ELISA based assays necessitate the use of antibodies raised against the protein or peptide sequence and may be used for the detection of antigen in tissue or serum samples (McIntyre C.A., Rees R.C. *et. al.*, Europ. J. Cancer 28, 58-631 (1990)). In-situ detection of antigen in tissue sections also rely on the use of antibodies, for example, immuno peroxidase staining or alkaline phosphatase staining (Gaepel, J.R., Rees, R.C. et.al., Brit. J. Cancer 64, 880-883 (1991)) to demonstrate expression. Similarly radio-immune assays may be developed whereby antibody conjugated to a radioactive isotope such as I^{125} is used to detect antigen in the blood (Turkes, A., *et.al.*, Prostate-specific antigen - problems in analysis. Europ. J. Cancer. 27, 650-652 (1991)).

Blood or tissue samples may be assayed for eleviated concentrations of the nucleic acid molecules, proteins or peptides.

Kits for detecting or monitoring cancer, such as prostate cancer, using polypeptides, nucleic acids or antibodies according to the invention are also provided. Such kits may additionally contain instructions and reagents to carry out the detection or monitoring.

The fourth aspect of the invention provides for the use of nucleic acid molecules according to the first aspect of the invention or protein/peptide molecules according to the second aspect of the invention in the prophylaxis or treatment of cancer, or pharmaceutically effective fragments thereof. By pharmaceutically effective fragment, we mean a fragment of the molecule which still retains the ability to be a prophylactant or to treat cancer. The cancer may be prostate cancer.

The molecules are preferably administered in a pharmaceutically amount. Preferably the dose is between 1 μg/kg. to 10 mg/kg.

The nucleic acid molecules may be used to form DNA-based vaccines. From the published literature it is apparent that the development of protein, peptide and DNA based vaccines can promote anti-tumour immune responses. In pre-clinical studies, such vaccines effectively induce a delayed type hypersensitivity response (DTH), cytotoxic T-lymphocyte activity (CTL) effective in causing the destruction (death by lysis or apoptosis) of the cancer cell and the induction of protective or therapeutic immunity. In clinical trials peptide-based vaccines have been shown to promote these immune responses in patients and in some instances cause the regression of secondary malignant disease. Antigens expressed in prostate cancer (or other types of cancers) but not in normal tissue (or only

weakly expressed in normal tissue compared to cancer tissue) will allow us to assess their efficacy in the treatment of cancer by immunotherapy. Protein or peptide derived from the tumour antigen may be administered with or without immunological adjuvant to promote T-cell responses and induce prophylactic and therapeutic immunity. DNA-based vaccines preferably consist of part or all of the genetic sequence of the tumour antigen inserted into an appropriate expression vector which when injected (for example via the intramuscular, subcutaneous or intradermal route) cause the production of protein and subsequently activate the immune system. An alternative approach to therapy is to use antigen presenting cells (for example, dendritic cells, DC's) either mixed with or pulsed with protein or peptides from the tumour antigen, or transfect DC's with the expression plasmid (preferably inserted into a viral vector which would infect cells and deliver the gene into the cell) allowing the expression of protein and the presentation of appropriate peptide sequences to T-lymphocytes.

Accordingly, the invention provides a nucleic acid molecule according to the invention in combination with a pharmaceutically-acceptable carrier.

A further aspect of the invention provides a method of prophylaxis or treatment of prostate cancer comprising the administration to a patient of a nucleic acid molecule according to the invention.

The protein/peptide molecules according to the invention may be used to produce vaccines to vaccinate males against prostate cancer.

Accordingly, the invention provides a protein or peptide according to the invention in combination with a pharmaceutically acceptable carrier.

The invention further provides use of a protein or peptide according to the invention in a prophylaxis or treatment of a cancer such as prostate cancer.

Methods of prophylaxis or treating prostate cancer, by administering a protein or peptide according to the invention to a patient, are also provided.

Vaccines comprising nucleic acid and/or proteins and peptides according to the invention are also provided.

The proteins and peptides of the invention may be used to raise antibodies. In order to produce antibodies to tumour-associated antigens procedures may be used to produce polyclonal antiserum (by injecting protein or peptide material into a suitable host) or monoclonal antibodies (raised using hybridoma technology). In addition PHAGE display antibodies may be produced, this offers an alternative procedure to conventional hybridoma methodology. Having raised antibodies which may be of value in detecting tumour antigen in tissues or cells isolated from tissue or blood, their usefulness as therapeutic reagents could be assessed. Antibodies identified for their specific reactivity with tumour antigen may be conjugated either to drugs or to radioisotopes. Upon injection it is anticipated that these antibodies localise at the site of tumour and promote the death of tumour cells through the release of drugs or the conversion of pro-drug to an active metabolite. Alternatively a lethal effect may be delivered by the use of antibodies conjugated to

radioisotopes. In the detection of secondary/residual disease, antibody tagged with radioisotope could be used, allowing tumour to be localised and monitored during the course of therapy.

The term "antibody" includes intact molecules as well as fragments such as Fa, $F(ab')_2$ and Fv.

The invention accordingly provides a method of treating prostate cancer by the use of one or more antibodies raised against a protein or peptide of the invention.

The cancer-associated proteins identified may form targets for therapy.

The invention also provides nucleic acid probes capable of binding sequences of the invention under high stringency conditions. These may have sequences complementary to the sequences of the invention and may be used to detect mutations identified by the inventors. Such probes may be labelled by techniques known in the art, e.g. with radioactive or fluorescent labels.

The invention will now be described by reference to the following figure and examples:

Figure 1 shows RT-PCR of different tumour samples showing over-expression of MTA-1 (SEQ.ID.57).

Technique used to identify genes encoding tumour antigens (SEREX technique)

The technique for the expression of cDNA libraries from human prostate cancer tissue is described, and was performed according to published methodology (Sahin et.al. Proc Natl. Acad. Sci. 92, 11810-11813, 1995).

SEREX has been used to analyze gene expression in tumour tissues from human melanoma, renal cell cancer, astrocytoma, oesophageal squamous cell carcinoma, colon cancer, lung cancer and Hodgkin's disease. Sequence analysis revealed that several different antigens, including HOM-MEL-40, HOM-HD-397, HOM-RCC-1.14, NY-ESO-1, NY-LU-12, NY-CO-13 and MAGE genes, were expressed in these malignancies, demonstrating that several human tumour types express multiple antigens capable of eliciting an immune response in the autologous host. This represents an alternative and more efficient approach to identify tumour markers, and offers distinct advantages over previously used techniques:

1) the use of fresh tumour specimens to produce the cDNA libraries obviates the need to culture tumour cells *in vitro* and therefore circumvents artefacts, such as loss or neo-antigen expression and genetic and phenotypic diversity generated by extended culture;

2) the analysis is restricted to antigen-encoding genes expressed by the tumour *in vivo*;

3) using cDNA expression cloning, the serological analysis (in contrast to autologous typing) is not restricted to cell surface antigens, but covers a more extensive repertoire of cancer-associated proteins (cytosolic, nuclear, membrane, etc.);

4) in contrast to techniques using monoclonal antibodies, SEREX uses poly-specific sera to scrutinise single antigens that are highly enriched in lytic

bacterial plaques allowing the efficient molecular identification of antigens following sequencing of the cDNA. Subsequently the tissue-expression spectrum of the antigen can be determined by the analysis of the mRNA expression patterns using northern blotting and reverse transcription-PCR (RT-PCR), on fresh normal and malignant (autologous and allogeneic) tissues. Likewise, the prevalence of antibody in cohorts of cancer patients and normal controls can be determined.

Construction of cDNA expression libraries, screening and sequencing

The detailed methodology for SEREX expression cloning established by the inventors is as follows: Total RNA is isolated from fresh prostate cancer tissues using the guanidinium thiocyanate-phenol-chloroform extraction method; RNA integrity is determined by electrophoresis in formalin/MOPS gels. Poly(A)+ RNA is prepared by applying the prepared RNA sample to a column of oligo (dT) cellulose and cDNA expression libraries is constructed from 5-8 μg of poly(A)+ RNA; first-strand synthesis is performed using an oligo(dT) primer with an internal *Xho* I site and 5-methyl-CTP. cDNA is ligated to *Eco*RI adaptors and digested with *Xho* I and cDNA fragments are cloned directionally into the bacterophage expression vector, packaged into phage particles, and used to transfect *Escherichia coli*. Immuno-screening for the detection of clones reactive with antibodies present in diluted autologous serum is then performed. Transfection for primary screening and plaque transfer onto nitrocellulose membranes is followed by pre-incubation of the membranes with an alkaline phosphatase-conjugated antibody specific for human IgG. Reactive clones representing expressed IgG heavy chains visualized by staining are eliminated from the study. These pre-stained membranes are then incubated with the autologous patient serum, and binding to recombinant proteins expressed in lytic plaques

detected by incubation with an alkaline phosphatse-conjugated goat anti-human IgG, and differentiated from the IgG-heavy chain transcripts. The reactive clones are sub-cloned, purified, and *in vitro* excised to pBK-CMV plasmid forms. Plasmid DNA is prepared using the Wizard (Trade Mark) Miniprep DNA purification system (Promega Corp., Southampton, UK). The inserted DNA is evaluated by restriction mapping, and clones representing different cDNA inserts sequenced using the automated sequencer.

Expression of Antigens in Different Cancers

The expression of metastasis associated 1 (MTA1) (SEQ.ID.57) in cancer samples was compared with that in corresponding normal tissues by semi-quantitative reverse-transcription polymerase chain reaction (RT-PCR). RT-PCR was carried out using processes well known in the literature. A relative over-expression of MTA1 mRNA (normal/tumour ratio$\geq$2) was observed in esophageal cancer (3/7) and head and neck tumour (1/7) (Table 1). See Figure 1, tracks 6 and 8. Testis did not show any over-expression. GAPDH (Glyceraldehyde-3-phosphate Dehydrogenase) expression was also tested as a control. No difference in expression was normal tissue and observed between tumours.

Table 1

Tumour type	Positive rate
Esophageal cancer	3/7
Head and neck tumour	1/7

Table 2 shows the results of further studies of a variety of sequences in different tumours. " – " indicates not studied. This table shows that the proteins are immunogenic in a higher portion of patients with cancer than controls since the patients have antibodies against the cloned protein product.

Table 2

Serological responses in cancer patients and controls to the protein products of genes cloned from the cDNA library using SEREX.

SEQ ID #	Gene size bp	Identity	*Immunoscreening with sera from :* Controls	BPH	Prostate Ca	Head & Neck Ca	Co Ca	Ga Ca
8	Pr III-41 3500 137,144	Unknown	0/7	-	4/10	2/4	-	-
10	Pr III-90 3000 102,108	Unknown	0/10	0/2	2/7	2/4	-	-
12	Pr III-104 1500	Unknown	0/8	0/2	2/7	2/4	-	-
16	Pr III-133 1550	Unknown	0/5	0/2	4/7	-	-	-
18	Pr III-147 1100	Unknown	1/10	0/2	8/12	2/4	0/2	-
50	Pr III-157 400	Hu Ribosomal Protein S10	0/4	-	5/10	1/4	-	-
57	Pr III-176 2600	MTA1	0/13	0/3	2/13	-	0/2	0/2
60	Pr III-197 1200	ALG2	1/17	0/3	4/13	3/4	0/2	0/2
29	Pr III-213 2500	Unknown	0/6	0/2	4/12	2/4	0/2	-

Serum samples from:
Controls
BPH- Benign Prostatic Hyperplasia
Prostate Cancer
Head and Neck Cancers
Co Ca-Colon Cancer
Ga Ca-Gastric Cancer

Table 3 shows some of the mutations identified by the inventors.

Table 3

SEQ ID #	Gene	Identity	Mutation
35	PrIII-30	Human geminin.	Point mutation at nt 78 (A to C)
34	PrIII-13	Human glutamyl-prolyl-tRNA synthetase	261 nt longer at 5' of mRNA. There is a starting code (ATG) in this region. This clone may be a new isoform.
43	PrIII-118	Human poly(ADP-ribose) polymerase mRNA.	Point mutation at nt 79 (C to G) and nt 145 (G to A).
44	PrIII-119	Human tankyrase	Point mutation at nt 2410 (G to A).
52	PrIII-163	Human mitochodrial DNA	Point mutation at nt 10769 (A to G).
60	PrIII-197	Human calcium binding protein (ALG-2) mRNA.	6 nt deletion from nt 487 to 492 (GGTTTC).
65	PrIII-219	Human FACL5 for fatty acid coenzyme A ligase 5	Point mutation at nt 758 (A to G)
66	PrIII-224	Human DNA-binding protein (HRC 1) mRNA	129 nt deletion in exon 2. This clone may be an alternatively spliced isoform.

Mutations detected in the sequence of genes cloned by SEREX.

SEQ ID 1
PR2-7A Human mRNA for KIAA0160 gene
GGCGGCTCGGGGCCCAGCGCGGGGTCCGGGGGAGGCGGCTTCGGGGGTTCGGCGGCGGT
GGCGGCGGCGACGGCTTCGGGCGGCAAATCCGGCGGCGGGAGCTGTGGAGGGGGTGGCA
GTTACTCGGCCTCCTCCTCCTCCTCCGCGGCGGCAGCGGCGGGGGCTGCGGTGTTACCGGT
GAAGAAGCCGAAAATGGAGCACGTCCAGGCTGACCACGAGCTTTTCCTCCAGGCCTTTGA
GAAGCCAACACAGATCTATAGATTTCTTCGAACTCGGAATCTCATAGCACCAATATTTTTG
CACAGAACTCTTACTTACATGTCTCATCGAAACTCCAGAACAAACATCAAAAGGAAAACA
TTTAAAGTTGATGATATGTTATCAAAAGTAGAGAAAATGAAAGGAGAGCAAGAA

SEQ ID 2
PR2-1A Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA
ACAGGTGAAAAACCAAATACTTTCTAGGGATGACCTTGATGACATAATTCAGTCATCTCA
AACAGTCTCAGAGGACGGTGACTCGCTTTGCTGTAATTGTAAGAATGTCATATTACTCATT
GATCAACATGAAATGAAGTGTAAAGATTGTGTTCACCTATTGAAAATTAAAAAGCATTTT
GTTTATGTAAAAGATTAACAGAACTTAAAGATAATCACTGTGAGCAACTTAGAGTAAAAA
TTCGAAAACTGAAAAATAAGGCTAGTGTACTACAAAAGAGACTATCTGAAAAAGAAGAA
ATAAAATCGCAGTTAAAGCATGAAACACTTGAATTGGAAAAAGAACTCTGTAGTTTGAGA
TTTGGCCTACAGCAAGAAAAAAAGAAAAGAAGAAATGTTGA

SEQ ID 3
PR2-21 2 Human JK-recombination signal binding protein (RBPJK) gene
GAGAGTTTGTGGAAGATGGCGCCTGTTGTGACAGGGAAATTTGGTGAGCGGCCTCCACCT
AAACGACTTACTAGGGAAGCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGT
ACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAATGAAAAAAGGTTTTTTTGC
CCACCTCCTTGTGTATATCTTATGGGCAGTGGATGGAAGAAAAAAAAAGAACAAATGGAA
CGCGATGGTTGTTCTGAACAAGAGTCTCAACCGTGTGCATTTATTGGGATAGGAAATAGT
GACCAAGAAATGCAGCAGCTAAACTTGGAAGGAAAGACTATTGCACAGCCAAAACATTG
TATATATCTGACTA

SEQ ID 4
PR2-5A Human mRNA for E6-AP isoform-I
GATTCGGAGAATGATGGAGACATTTCAGCAACTTATTACTTATAAAGTCATAAGCAATGA
ATTTAACAGTCGAAATCTAGTGAATGATGATGATGCCATTGTTGCTGCTTCGAAGTGCTTG
AAAATGGTTTACTATGCAAATGTAGTGGGAGGGGAAGTGGACACAAATCACAATGAAGA
AGATGATGAAGAGCCCATCCCTGAGTCCAGCGAGCTGACACTTCAGGGAACTTTTGGGAG
AAGAAAGAAGAAACAAGAAAGGTTCCTCGAGTGGACCCCCTGGAAACTGAACTTGGTGTT
AAAACCCTGGATTGTCGAAAACCACTTATCCCTTTTGAAGAGTTTATTAATGAACCACTGA
ATGAGGTTCTAGAAATGGATAAGATTTACTTTT

SEQ ID 5
PR2-20 3 Human mRNA for TPRD
GGAATATGTCTTACCCCTGACTGTGAAGGTGTCATTTCTAAGATTATCATCTTCAGCAGTG
GTGGTGAAGTTAAATGTGAATTTGAACACAAGGTCATAAAAGAAAAGGTTCCTCCAAGAC
CTATTCTGAAACAGAAATGTTCTAGCCTAGAGAAACTAAGACTGAAAGAAGACAAAAAAT
TGAAGAGAAAGATCCAAAAAAAAAGAAGCAAAAAAGTTAGCACAAGAAAGAATGGAGGA
GGACTTAAGAGAAAGTAATCCACCCAAAAATGAAGACAGAAAGAAACTGTAGACAATGT
TCAAGCGTTGTCAGTTCCTTGATGACAGAATTCTACAGTGTATAAAGCAGTATGCTTGACA
GGATTAAATCCGGCATACAGAATACAGCCATGCTTCTAAAGAATTGTTT

SEQ ID 6
PR2-1B Unknown
GGGAAGCAGAAGGATTTGGAGTTTCTTTTTAAAGTGATTCCTTCCTTTCCCCTTTCATTTTT
CCACTGTGGGTGTTATTATCCTGACAATTTGTCATACATTTCCTGTCTTTAAAAAATAACTG
TATACTAAGCAAAACTCAGGTCTTAAAAATAAATATGAATTTAGATTCCATACATCGATTA
ATTGAGGAAACACAGATCTTCCAGATGCAACAATCATCAATTAAGTCACGCGGCGACATG
GTGGCCCCTGCCTCACCCCCCAGGGATACCTGTAATACCTGCTTCCCACTTCATGGGCTAC
AATCTCATGCTGTCACAATTTCTGTGCTCACTCATATAACACCACAAATGGGATATTTGTG

AAGAACTTCGCTGCGGAGCT

SEQ ID 7
PR2-2 Unknown
AGGGACAGCTCTTGCATCGAGACCCCTTCACTGTCATCTGTGGCCGAAAGAAGTGCCTTCG
CCATGTCTTTCTCTTCGAGCATCTCCTCCTGTTCAGCAAGCTCAAGGGCCCTGAAGGGGGG
TCAGAGATGTTTGTTTACAAGCAGGCCTTTAAGACTGCTGATATGGGGCTGACAGAAAAC
ATCGGGGACAGCGGACTCTGCTTTGAGTTGTGGTTTCGGCGGCGGCGTGCACGAGAGGCA
TACACTCTGCAGGCAACCTCACCAGAGATCAAACTCAAGTGGACAAGTTCTATTGCCCAG
CTGCTGTGGAGACAGGCAAGCCCACAACAAGGAGCTCCGAGTGCAGCAGATGGTGTCATG
GCATTGGGAATAAACCCTTCTGGACATAAAGCCCTTGGGGAGCGA

SEQ ID 8
Pr3-41 Unknown
GCGGCGGCGGCCCCTCGCAGCAGCTGGCCGGCGGGCCCCCCCAGCA
GTTCGCGCTCTCCAACTCCGCGGCCATCCGGGCCGAGATCCAGCGCT
TCGAGTCCGTGCATCCCAATATCTACGCCATCTACGACCTGATCGAGC
GCATCGAGGATTTGGCGCTGCAGAACCAGATCCGGGAGCACGTCATC
TCCATCGAGGACTCGTTTGTGAACAGCCAGGAGTGGACGCTGAGCCG
CTCCGTACCGGAGCTTAAAGTGGGCATAGTGGGGAACCTGTCTAGCG
GGAAGTCAAGCCCTGGTGCACCGCTATCTGACGGGGACCTATGTCCA
GGAGGAGTCCCCTGAAGGGGGGCGGTTTAAGAAGGAGATTGTGGTG
GATGGCAGAGTTCCTGCTGTGATC

SEQ ID 9
Pr3-42 Unknown
GGCTGGCAGTAGAGGTGACCGAGGCGGTGGCGGCGGAGGCGGCACC
GATTGCTGTGTCGGCCCCAGTGCGGCCGAAGTCGCGGTAGAGCGTAG
CCCCACGCCCCTCCCCCGTCCGCGCCCTCCCTCTTTCCCTGGGGATG
GAGAAGGCGACGGTTCCTGGTGGCGGCGGCGACGGCTTGCAGAAGG
AGAAGGGAGCCCCCCGGCGGTGGCGGCTTGTGGCGGGCCCCCCCGC
GGCGGCGGAGGTCGGCGGCGGCGTTGGCGGCAGCAGCAGAGCTCGC
TCGGCCTCGTCTCCTCGTGGGATGGTGCGAGTCTGCGACCTGCTCCT
GAAGAAGAAGCCGCCGCAGCAGCAGCACCACAAGGCCAAGCGTAAC
CGGACTTGCCACCCCCCAGCAGCAGCGAAAC

SEQ ID 10
Pr3-90 Unknown
GCGGCGGCGGCCCCTCGCAGCAGCTGGCCGGCGGGCCCCCCCAGCA
GTTCGCGCTCTCCAACTCCGCGGCCATCCGGGCCGAGATCCAGCGCT
TCGAGTCCGTGCATCCCAATATCTACGCCATCTACGACCTGATCGAGC
GCATCGAGGATTTGGCGCTGCAGAACCAGATCCGGGAGCACGTCATC
TCCATCGAGGACTCGTTTGTGAACAGCCAGGAGTGGACGCTTGAGCC
GCTCCGTACCGGAGCTTAAAGTGGGCATAGTGGGGAACCTGTCTAGC
GGGAAGTCAGCCCTGGTGCACCGCTATCTGACGGGGACCTATGTCCA
GGAGGAGTCCCTGAAGGGGGGCGGTTAAGAAGGAGATTGTGGTGGA
TGGCAGAGTTCCTGCTGC

SEQ ID 11
Pr3-93 Unknown
ATTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAAATG
CAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTCTAAGA
ACAGGGTTGAAGTATGTTCTCTTCTCTTAAGTTATGGTGCAGACCCAA
CACTGCTCAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACAC
CACAGTTAAAAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGC

TGCAAGCTGCACGAGAAGCTGATGTTACTCGAATCAAAAAACATCTCT
CTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAACAGCAT
TGCATTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAAATATGTG
AACTGTTGCTAGAAAAGC

SEQ ID 12
Pr3-104 Unknown
CCTCAGCATACCCACCGAGCAGCTGCCAGCCTGGGCTGAGGGTGGGC
ATGAGGCAGGAGTCAGCACTTGGACCTAGGGATGTGAGGTTTTCTGT
GCCCCAAGTTTGTGGGAAGGTGGGCACTACTGCTGGGCCCACAGACA
CAGCCAGCTGGCAAAAGGGAGGTCTAGCCCAGCAGAGAGATGAGGA
CATTTTGCTTCTCCTTCATGCCCACAGCATGAGCTGAGCTTCTGCTTT
GCTGGAAATGAAATAAACTTGGTATGAATTGTGCCAAGGCCTCCCCA
GTTGTCATCCTGCCTCTTGTTGCCCTCCCTTGTCCTTGCCCCCCACCC
CACACCCATGCCCCTGTTTCCTTACAGATTTTGATATTGTCTAATGTG
TAATAGAACCAGCCGAGTCCCA

SEQ ID 13
Pr3-113 Unknown
CTTACCTCATTTCTGAATGTGCATTTCCAGCCTTCTTGCTCTCAGAGC
TATTGTTCAAGCAGAAAACAAGCTGCTTTTATTACA

SEQ ID 14
Pr3-122 Unknown
GAGAGAACTAGTCTCGAGTTTTTTTTTTATTCTTCTATATTCTATGAAT
ATGGTGCTGTCCTGTCATTTAATTATTATAATATATGTGAACTGCTGG
AGGTAAA

SEQ ID 15
Pr3-124 Unknown
TCGATCCTTAGTGACTTAACAATCAGGCCTTAATTGAAACACACACAC
ACATTGTTATTGACAGTGTAGAAATACTGACTCATAGAAAAATTCACC
CATATTTAGTTAGCAGACTAACAGGAACAGCAGCAGCAGCAGCAGCT
GGTCATGCTTCTGTGTGTTGCTAGCAACAAGAAACCATGACAGCAAG
GCCCCAAACAGGAACCTCCTGCATTTTCTCATCTGTGATGAGGCACAC
TTGATGCTGGGGATTAATGAGCCTGAAGATATAAAGCAGTGTTTACC
ACTGGAAAATGTCTCCTACACTAAAAGCAGAGGTAAGTATCAATGCA
AACCGAGTGCAGCTATAAAGCCTTGATTTCTCTGGAAATTATGTACAA
ACTAATACAAATAATCTCATTACTTGAAAC

SEQ ID 16
Pr3-133 Unknown
GCTACGGCTGCTCCGGAGCTGGTGGCGCCGCGATAGGAGAGCCGAT
GGCCAAGTGGGGTGAGGGAGACCCACGCTGGATCGTGGAGGAGCGG
GCGGACGCCACCAACGTCAACAACTGGCACTGGACGGAGAGAGATGC
TTCAAATTGGTCCACGGATAAGCTGAAAACACTGTTCTTGGCAGTGCA
GGTTCAAAATGAAGAAGTCAAGTGTGAGGTGACGGAAGTGAGTAAGC
TTGATGGAGAGTCATCCATTAACAATCGCAAAGGGAAACTTATCTTCT
TTTATGAATGGAGCGTCAAACTAAACTGGACAGGTACTTCTAAGTCAG
GAGTACAGTACAAAGGACATGAGGAGATCCCCAATTTGTCTGATGAA
AAC

SEQ ID 17
Pr3-140 Unknown
CATTACCTTACAGTGTAAACAGGAGTCTAATTTGTATCAATACTATGT
TTTGGTTGTAATATTCAGTTCACTCACCCAATGTACAACCAATGAAAT
AAAAGAAGCATTTAAAAGGAA

SEQ ID 18
Pr3-147 Unknown
GGCGTGTGGGTCTCGCAGCGTTGCTCACAGAACAGAGTAGAGGCGGC
GGCGGCGGCGGCCGGACCCAGACTGGTAGTGAGGCGTTGGACCCCG
AGCCGCTGCAATGCCGCTGGAGCTGGAGCTGTGTCCCGGGCGCTGG
GTGGGCGGGCAACACCCGTGCTTCATCATTGNCGAGATCGGCCAGAA
CCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATCCGCATGGCCA
AGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAA
TTCAAGTTTAATCGGAAAGCCTTGGACAGGCCATACACCTCGAAGCA
TTCCTGGGGGAAGACGTACGGGGAGCACAAACGACATCTGGAGTTCA
GCCATGACCAGTCAGGGAGCTGAGAGGTCC

SEQ ID 19
Pr3-148 Unknown
GACGGACCGAGACCGGAGATGTTTTCAAGCCCGGCTCCGGCGGCTTT
ACAGGCGGCTGCAGCGGCGACGAAGACAACGACAGCGACGGCTACG
CCGAAGCACTCGAACCGGGGGTGAAGCCTCCTGCGCCGGCCTTGCCT
CGGATCCAGGATGAGAAGACTGATAAAAGAAGAAGCTAGCTGAACAG
CTGTAAAATGCCCAAATCTGGGTTCACAAAACCAATTCAGAGTGAAAA
TTCTGACAGTGACAGCAATATGGTAGAGAAACCATATGGAAGAAAGA
GTAAAGACAAGATTGCATCCTACAGCAAAACTCCAAAAATTGAACGA
AGTGATGTGAGCAAGGAGATGAAAGAGAAATCATCCATGAAACCGTA
AACTTCCTTTC

SEQ ID 20
Pr3-162 Unknown
GCAGGAGGGGCCTTGCCAGCTTCCGCCGCCGCGTCGTTTCAGGACCCGGACGGCGGA
TTCGCGCTGCCTCCGCCGCCGCGGGGCAGCCGGGGGGCAGGGAGCCCAGCGAGGGGC
GCGCGTGGGCGCGGCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCG
GCCGGGCCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCCTGCTCGCGGGGCCGG
GGCTCCTGCTCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGCGGCCAGGATCATGT
CGGGTCGCCGCTGCGCCGGCGGGGGAGCGGCTGCGCGAGCGCCGCGGCCGAGGCCGT
GGAGCCGGCCGCCGAAGCTGTTCGAGGCGTGCCGAACGGGGACGTGGAACGAGTAAG
AGGCTG

SEQ ID 21
Pr3-180 Unknown
GCCAACTCAGTCCAGCAGAACAAAATGTAGCTGCCATTCTTGGAGTC
TCTGAAAGCTTTATTGGGAAGAAAGCATCAGGCCAAGCCATCGGAAA
GAAGGTGGACAAGAACGTTGTCAACAGGCTATATCTGTCTTTTGTTCT
TTATACCTTGCTCAAAGAGACCAACATTTGGACTGTATCTGAAAAATT
TAATATGCCTCGAGGATATATACAAAATCTTCTCACTGGAACTGCCTC
ATTCTCATCTTGTGTGTTACATTTCTGTGAGGAGCTTGAGGGAGTTTT
GGGTTTACAGAGCCCTTTTGGTAGAACTTACCAAGAAGCTGACTACT
GTGTAAAGGGCAGAATTAATCCCTCTATGGGAAGTTCTNGGAGTTTTA
GAGGGTCGAGCAAAACAGTTTTTCAGNGCCNGGTACCAAAAGTCTAA
TGCCTTAGCTAAGCAAACCCTGAANGNTTCTANGGNCAATTGGTCNTT
TTTTAAGACCCCAAGCCAGCAAATTGTTTATNCAAAAATCTNTTCNTN
AAAACCAAACCTCAAAANGGNNAAAAGTCCNAAATGCTTTTNTTCCCG
GGGGNGGGGGTTNTTCCCGGCAAACNGAANTTTTTGNGGGAANTTTT
TTTTAATTTTTTTNG

SEQ ID 22
Pr3-187 unknown
GGGAGGCGGCGGCAGCGTTAAGTGAGAAAGGAAAAAAGACAACGAGGAAAAAGGAGG
TGTCCGGGTAGGGCAACGCGGCGACACCCGAGGCCTGGTGGTGGCGGCGGATCGAGA
TATTCAAGGCTGAAGCAGCTACGGAACGGCAGCGGCGGCGGTCGGACAAACTGACTG

ACCGAGCCGGGTGGTGGCGGGAGCAGCGGGAGCAGCCGGAACGATGCCGGCCGTGAG
CCTCCCGCCCAAGGAGAATGCGCTCTTCAAGCGGATCTTGAGGTGTTATGAACATAA
ACAGTATAGAAATGGATTGAAATTCTGTAAACAAATACTTTCTAATCCCAAATTTGC
AGAGCATGGAGAAACCTTGGCTATGAAAGGATTAACATTGAACTGTTTGGGGAAAAA
GGAAGAACTTATGAATTGGTTCCTAGAGGTTTGAGAAATGACTTGAAGAGTCATGTG
TGTTGGCCACGTTTATGGCCTTTTTCAAGGTCANACAAGAAGTNTGATGAANNCCTT
AANTGTTACAGAAATGCCTAAATGGGATAAGACATCTTAAATTTTAAGGGNCTTTCT
TCTACAANTCAATCCAAACTNGNGGNTTCCNGGAACCAGGTTTNANTTCTTCANTTN
CNCCTCCCAAAGCATTATGNT

SEQ ID 23
Pr3-194 Unknown
CGGTGGCGGCGGAGGCGGCACCGATTGCTGTGTCGGCCCCAGTGCGGCCGAAGTCGC
GGTAGAGCGTAGCCCCACGCCCCTCCCCCGTCCGCGCCCTCCCTCTTTCCCTGGGGA
TGGAGAAGGCGACGGTTCCGGTGGCGGCGGCGACGGCTGCAGAAGGAGAAGGGAGCC
CCCCGGCGGTGGCGGCTGTGGCGGGCCCCCCCGCGGCGGCGGAGGTCGGCGGCGGCG
TTGGCGGCAGCAGCAGAGCTCGCTCGGCCTCGTCTCCTCGTGGGATGGTGCGAGTCT
GCGACCTGCTCCTGAAGAAGAAGCCGCCGCAGCAGCAGCACCACAAGGCCAAGCGTA
ACCGGACTTGCCGACCCCCCCAGCAGCAGCGAAAGCAGCAGCGACAGCGACAACAGCG
GCGGCGGTGGAGGCGGCGGTGGAGCGGAAGTGGCGGCGGCGGCACCAGCANTAACAA
CAGCGAGGAAANAAAGGACACACACCAGGAANAGAGGTTNTGAGGGGAGTTTTATTT
GGNTCAGATTATTGGAAANTCAANCTTGNAAACTTCCAGGTNNTCTATAANGTCNNT
TGTNGNGCATACNTANGAANTANNCCAAAANNAGNTTTNATGGGAGTTTTACNAAAC
NCAGTTTGGATC

SEQ ID 24
Pr3-199 Unknown
CTNNGTTTTTTTTTTTTTTTTTTCCAGACTCTTCTGTTCTTTTATATCTCAGAAAG
GATTGGGTTTTCAGGTTGCAAAATCTTTTCCAGCTCTGCATAGGTAGGTAGCATCTC
ACTGAGGAATGGAGTATTTACCACCTATTGTTCTGTNCCAGTCTAGTAGAGCTTTAG
CAAAANCTACAGGCAACAAATTCTATTTTTAACATCCTGTTACACAAACAAATATGC
TGAGTATGCACACAAATAAATGGTGAAAGAGGCNCAAAGAAGTGAAAACAATCGTGC
ATGGTAGGAATATTTGAATTGTNTTACATGTCCTTTAATATTGNTTTAACAGTNATA
TTTTTACATTTTCAATTGGAATGAAAAGCATGTCTGTGTTCGAATAATTTTTCATCG
NNCNCTCATTTTTTTGATTCCCNANCTAATGAGNAGAAANCAGTGATGATTGCAAAA
TGTTTCCCNCCCTNAAGGAATNCNCGTNNGAATTCTTGCAGNTCCTGGAGANCTCCN
TANTTTANGNCNTATATAGGTANNGATCTATACTCCCTCGGGGGGTCTTAGCCTNNC
GCNNCCTNCCTTCCNTCTCACNANCATTGTTNTCTANNGCNNCTCANNTAANTNCTN
CAGGCCCNCAANTGNNTATNNANCCNCNNNCNTNTC

SEQ ID 25
Pr3-201 Unknown
CCCGGAACCTGCAAGGCCTGGTCTGGGACCCACACAACCGTAGGAGA
CAGGTCCTGAATACCCGGGCCCAAGAGCCCAAGCTGTGCTGGCCTCA
GGGTTTCTCCTGGAGTCACCGAGCCGTGGTCCACTTCGTCGTGCCTG
TGAAGAACCAGGCACGCTGGGTACAGCAATTCATCAAAGACATGGAA
AACCTGTTCCAGGTCACCGGTGACCCACACTTCAACATCGTCATCACT
GACTATAGCAGTGAGGACATGGATGTTGAGATGGCACTGAAGAGGTC
CAAGCTGCGGAGCTACCAGTACGTGAAGCTAAGTGGAAACTTTGAAC
GCTCAGCTGGACTTCAGGCTGGCATAGACCTCGTGAAGGACCCGCAC
AGCATCATCTTCCTcTGTGACCTCCACATCACTTCCCACTTGGAGTCA
TNGATGCCATTCGGAACACTTGTGTGGAGGGAAAAGAAGGGCTTTTG
CCCCCTGGTGATAAGGTTGNNTTGGGGGCNCCCCCAANGGCTGAGGC
TCGGGAGGGAAAAGGGTTGGGNNTTGGATTTACAATTTNCCTGANAN
GATGGGGGCNTAACCAAAAGGANTCCAAANCCTGGGNGGGAAAAANG
GNACTTTTNNAGGAATTTCAANGCN

SEQ ID 26
Pr3-202 Unknown
GTGAGATGAATGTTCCCCCTTCAATTCTCCTTATTTGCCAAATATTTT
CATTTCCTTTTGTCATTATAGAAAATAAAACCATGCATCACA

SEQ ID 27
Pr3-205 Unknown
AGGAACCAAAGAAGACATGGTCCCTGTCCTCATGGTTCAGACAGGGAGGCAGACATT
AAACAACTAATTATCAGTTATTCAATTA

SEQ ID 28
Pr3-208 Unknown
GCGACTCGGGGACCTGGAGCTGACGCCTAGACACTTGTATTAGCTTT
AATAGAAGAGAAATGGAGGAGCCATAGAATATTAAGGATGAATTCAG
GAAGGCCTGAGACCATGGAAAACTTGCCTGCTCTCTACACTATTTTCC
AAGGAGAGGTTGCTATGGTGACAGACTATGGGGCCTTTATCAAAATC
CCAGGCTGTCGGAAGCAAGGTCTGGTCCATCGAACTCATATGTCATC
CTGTCGGGTGGATAAGCCCTCTGAGATAGTAGATGTTGGAGATAAAG
TGTGGGTGAAGCTTATTGGCCGAGAGATGAAAAATGATAGAATAAAA
GTATCCCTCTCCATGAAGGTTGTCAATCAAGGGGACTGGGAAAGACC
TTGATCCCAACAATGTTATCATTGAGCAAGAAGAGANCGGAGGCGA
TCCTTCCAGGATTACACTGGGCAGNAAGATCACCCTTGAGGCTTGTCT
TGACCCTACCTCAANAAGNGNGGNTGTAAAGGGCCCTTTGCAAAAAA
TGGTTATGCANCNGGGGGAATTAAACTTTTTTTCCNTTGGGAAAGGAA
AGGAAAGCCAATCCCCANTTTGNAAACCTNCCTCAGGAATCTTTTAAA
NAAAGAGGGAAAAAAAANAACCN

SEQ ID 29
Pr3-213 Unknown
CTGTCATGGCTGCTCCTGTACGTAGTCACGGTCTTGTGCTCTAAGGAA
AACGACAGCACGTGTTCTTTTTCACTAGTAGAAGTGACGTTGGTTTCA
TGTTGACAACTTTGAAGCCATTTGGAAGTGTTTCAGTGGAGAACAAAA
TGAATAACAAAGCGGGCTCCTTTTTCTGGAACCTTAGACAATTCAGTA
CATTAGTTTCAACAAGCAGAACTATGAGGCTATGTTGTTTGGGACTTT
GCAAACCAAAAATAGTTCATTCAAACTGGAACATTTTAAATAACTTTC
ATAACAGAATGCAATCAACTGATATCATTAGATATCTCTTTCAGGATG
CATTCATTTTTAAATCAGATGTTGGCTTTCAAACAAAGGGCATAAGCC
TCTACAGCCCTTAGAATTGAAGAC

SEQ ID 30
Pr3-214 Unknown
GTATGGCGGCGTCAAAGGTGAAGCAGGACATGCCTCCGCCGGGGGG
CTATGGGCCCATCGACTACAAACGGAACTTGCCGCGTCGAGGACTGT
CGGGCTACAGCATGCTGGCCATAGGGATTGGAACCCTGATCTACGGG
CACTGGAGCATAATGAAGTGGAACCGTGAGCGCAGGCGCCTACAAAT
CGAGGACTTCGAGGCTCGCATCGCGCTGTTGCCACTGTTACAGGCAG
AAACCGACCGGAGGACCTTGCAGATGCTTCGGGAGAACCTGGAGGAG
GAGGCCATCATCATGAAGGACGTGCCCGACTGGAAGGTGGGGGAGT
CTGTGTTCCACACAACCCGCTGGGTGCCCCCCTTGATCGGGGAGCTG
TACGGCTTGCGCACCACAGAGGAGGCTCTTCATGCCAGCC

SEQ ID 31
Pr3-2 Homo sapiens geminin mRNA
GCAGGGCTTTACTGCAGAGCGCGCCGGGCACTCCAGCGACCGTGGG

GATCAGCGTAGGTGAGCTGTGGCCTTTTGCGAGGTGCTGCAGCCATA
GCTACGTGCGTTCGCTACGAGGATTGAGCGTCTCCACCCATCTTCTGT
GCTTCACCATCTACATAATGAATCCCAGTATGAAGCAGAACAAGAAG
AAATCAAAGAGAATATAAAGAATAGTTCTGTCCCAAGAAGAACTCTGA
AGATGATTCAGCCTTCTGCATCTGGATCTCTTGTTGGAAGAGAAAATG
AGCTGTCCGCAGGCTTGTCCAAAAGGAAACATCGGAATGACCACTTA
ACATCTACAACTTCCAGCCCTGGGGTTATTGTCCCAGAATCTAGTGAA
AATAAAATCTTGGAGGAGTACCCAGGA

SEQ ID 32
Pr3-8 Homo sapiens scaffold attachment factor A
GCGAACTCGGTGAAAGGAATTGGCGCCGTTCGACACCAGGCGGATCC
GCTCTGCAGCACGAACCCATCTCCAGCCGCAGCCGCAGCCGCCGCCC
GGGCCGAGGAGCAGCCGCAGCAGCCGCACCAGTGGCCGAGTGAGCG
GAGCCGAGTTTGAGGCAGCGCCTAGCGGTGAATCGGGGCCCTCACCA
TGAGTTCCTCGCCTGTTAATGTAAAAAAGCTGAAGGTGTCGGAGCTG
AAAGAGGAGCTCAAGAAGCGACGCCTTTCTGACAAGGGTCTCAAGGC
CGAGCTCATGGAGCGACTCCAGGCTGCGCTGGACGACGAGGAGGCC
GGGGGCCGCCCCGCCATGGAGCCCGGGAACGGCAGCCTAGACCTGG
GCGGGGATTCCGCTGGGA
SEQ ID 33
Pr3-11 Homo sapiens ribosomal protein L32
CCTACGGAGGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTC
AGACCCCTTGTGAAGCCCAAGATCGTCAAAAAGAGAACCAAGAAGTT
CATCCGGCACCAGTCAGACCGATATGTCAAAATTAAGCGTAACTGGC
GGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC
CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAAACAAA
GCACATGCTGCCCAGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCA
AGGAGCTGGAAAGTGCTGCTGATGTGCAACAAATCTTACTGTGCCGA
GATCGCTNACAATGTTTCTTCAAGACCGCAAAGCC

SEQ ID 34
Pr3-13 Homo sapiens glutamyl-prolyl-tRNA synthetase
GTCGGGTACGCGCACACGTTGCATCTTCTTCCTTTCGCGGGGTCCTC
CGTAGTTCTGGCACGAGCCAGGCGTACTGACAGGTGGACCAGCGGAC
TGGTGGAGATGGCGACGCTCTCTCTGACCGTGAATTCAGGAGACCCT
CCGCTAGGAGCTTTGCTGGCAGTAGAACACGTGAAAGACGATGTCAG
CATTTCCGTTGAAGAAGGGAAAGAGAATATTCTTCATGTTTCTGAAAA
TGTGATATTCACAGATGTGAATTCTATACTTCGCTACTTGGCTAGAGT
TGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGA
GATTGATCACTGGTTGGAGTC

SEQ ID 35
Pr3-30 Homo sapiens geminin mRNA (mutation at nt 220)
GCGGAGTTAGCAGGGCTTTACTGCAGAGCGCGCCGGGCACTCCAGCG
ACCGTGGGGATCAGCGTAGGTGAGCTGTGGCCTTTTGCGAGGTGCTG
CAGCCATAGCTACGTGCGTTCGCTACGAGGATTGAGCGTCTCCACCC
ATCTTCTGTGCTTCACCATCTACATAATGAATCCCAGTATGAAGCAGA
AACAAGAAGAAATCAAAGAGAATATAAAGACTAGTTCTGTCCCAAGA
AGAACTCTGAAGATGATTCAGCCTTCTGCATCTGGATCTCTTGTTGGA
AGAGAAAATGAGCTGTCCGCAGGCTTGTCCAAAAGGAAACATCGGAA
TGACCACTTAACATCTACAACTTCCAGCCTGGGGGTTATTGTCCCAGA
ATTCTAGTGAAAATAAAAATTTNGNNGGGAGTCACCCANGGAGTATTT
TTGATCTTATGATTAAAGGAAAATCCATCTTTTAATATTGAAGGGGAA
GNGGGCAGAAAAACGGAAAAGGGGNCCTTTNTGAAGCACTTAAGGGA
AAATGAGNAAACTTCATAAAGNAAATTGACCAAANGGACAATTGAAA
ATGGCCCGCTGAAAAAGGAAAATAAAGACTGGCNNNAAGTAGCAAAA

CATGTCCNGGTTTTTG

SEQ ID 36
Pr3-43 Homo sapiens DNA-binding protein (HRC1) mRNA
(5'end of the clone corresponds to the beginning
of exon 2 of HRC1)
CAGGCATGTTGTTGGGACTGGCGGCCATGGAGCTGAAGGTGTGGGTG
GATGGCATCCAGCGTGTGGTCTGTGGGGTCTCAGAGCAGACCACCTG
CCAGGAAGTGGTCATCGCACTAGCCCAAGCAATAGGCCAGACTGGCC
GCTTTGTGCTTGTGCAGCGGCTTCGGGAGAAGGAGCGGCAGTTGCTG
CCACAAGAGTGTCCAGTGGGCGCCCAGGCCACCTGCGGACAGTTTGC
CAGCGATGTCCAGTTTGTCCTGAGGCGCACAGGGCCCAGCCTAGCTG
GGAGGCCCTCCTCAGACAGCTGTCCACCCCCGGAACGCTGCCTAATT
CGTGCCAGCCTCCCTGTAAAGCCACGGGCTTGCGCTTGGGCTGTGAG
CCCCGCAAAACACTGACCCCGAGCCAGCCC

SEQ ID 37
Pr3-49 Homo sapiens vesicle docking protein p115 mRNA
CCGAGTTGGAGGCGGTGGAGCCAGCAGTAGGAGTGTGTAGAGTGCG
GGATTGGGGGCCAGGCCCTGCGGAGGGCGGGGGAAGTTGTCTTCTTT
TTTTTCCGGAGGGGCCGGTAAACCTGGTGGCTGAACGGCAAGATGAA
TTTCCTCCGCGGGGTAATGGGGGGTCAGAGTGCCGGACCCCAGCACA
CAGAAGCCGAGACGATTCAAAAGCTTTGTGACAGAGTAGCTTCATCT
ACTTTATTGGATGATCGAAGAAATGCTGTTCGTGCTCTCAAATCATTA
TCTAAGAAATACCGCTTGGAAGTGGGTATACAAGCTATGGAACATCTT
ATTCATGTTTTACAAACAGATCGTTCANATTCTGAAATTATAGGTATG
CTTTGGACACACTATATAATNNATATCTAA

SEQ ID 38
Pr3-101 Homo sapiens upstream transcription factor, c-fos interacting (USF2)
ACATGCTGGACCCGGGTCTGGATCCCGCTGCCTCGGCCACCGCTGCT
GCCGCCGCCAGCCACGACAAGGGACCCGAGGCGGAGGAGGGCGTCG
AGCTGCAGGAAGGCGGGGACGGCCCAGGAGCGGAGGAGCAGACAGC
GGTGGCCATCACCAGCGTCCAGCAGGCGGCGTTCGGCGACCACAACA
TCCAGTACCAGTTCCGCACAGAGACAAATGGAGGACAGGTGACATAC
CGCGTAGTCCAGGTGACTGATGGTCAGCTGGACGGCCAGGGCGACAC
AGCTGGCGCCGTCAGCGTCGTGTCCACCGCTGCTTCGCGGGGGGGCA
AGCAGGCTGTGACCAGGTG
GGTGTGC

SEQ ID 39
Pr3-109 Homo sapiens DNA-binding protein (HRC1) mRNA (Type I transcript)
GTCGGGGTGGGGCGTTCCCATGCCGGCGGCCGCGGGGCCTGGCGTG
CGGGCGCCTCCGCGCCGCCCGGGGAGGGGGCAGTGTCCTCCGAGCC
AGGACAGGCATGTTGTTGGGACTGGCGGCCATGGAGCTGAAGGTGTG
GGTGGATGGCATCCAGCTGTGTGGTCNTGTGGGGTCTCAGAGCAGAC
ACCTGCCAGGAAGTGGTCATCGCACTAGCCCAAGCAATAGGCCAGAC
TGGCCGCTTTGTGCTTGTGCAGCGGCTTCGGGAGAAGGAGCGGCAGT
TGCTTGCCACAAGAGTGTCCAAGTGGGCGCCCAGGCCACCTGCGGAC
AGTTTGCCAGCGATGTCCAGTTTGTCCTGAGGCGCACAGGGCCCAGC
CTAGCTGGGAGGCCTTCTAGACAGCTGC

SEQ ID 40
Pr3-111 Homo sapiens proteasome sub-unit HSPC mRNA
GAGTCGCGGCGGAAGGAGCCCGGCCGCCGCCCGCCGGCATGAGCTA
CGACCGCGCCATCACCGTCTTCTCGCCCGACGGCCACCTCTTCCAAG
TGGAGTACGCGCAGGAGGCCGTCAAGAAGGGCTCGACCGCGGTTGG
TGTTCGAGGAAGAGACATTGTTGTTCTTGGTGTGGAGAAGAAGTCAG

TGGCCAAACTGCAGGATGAAAGAACAGTGCGGAAGATCTGTGCTTTG
GATGACAACGTCTGCATGGCCTTTGCAGGCCTCACCGCCGATGCAAG
GATAGTCATCAACAGGGCCCGGGTGGAGTGCCAGAGCCACCGGCTGA
CTGTGGAGGACCCGGTCACTGTGGAGTACATACCCGCTACATCGCCA
GTCTGAAGCAGCGTTATACGCAC

SEQ ID 41
Pr3-112 Homo sapiens trans-Golgi p230 mRNA
GCCGAGGCCAGCCAGTGGCACCCGGAAGAAAGAGACGCGGCGGCGG
CGACGCCGACACCCTCAGGACGAGTGTCCGGACTTGCCCACAGCCTC
AAGGAGGAGACGGCGAGGCCCGGCCCCCGCTGTCCCTGGTGTAAAG
AAGTCGCCGTAGCCGTCGCGGCCGGGACTCCCCGGGCTCTCGCCCTT
CAGGTTTCGTTGACACTCAGGACCGTACGTACGCTTGCGCCATGTTC
AAGAAACTGAAGCAAAAGATCAAGCGAGGAGCAGCAGCAGCTCCAGC
AGGCGCTTGGCTCCTGCTCAGGCGTCCTCCAATTCTTCAACACCAACA
AGAATGAGGAGCAGGACATCTTCATTTCAGAGCAACTTGATGAAGGT
ACACCCAATAGAGAGTCAGGTGACACACAGTCTTTTGA

SEQ ID 42
Pr3-116 Homo sapiens ribosomal protein S14
CACCCCCATCCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTG
GTCGCCGTCTGTGAACAAGATTCCTCAAAATATTTTCTGTTAATAAAT
TGCCTTCATGTA

SEQ ID 43
Pr3-118 Homo sapiens poly (ADP-ribose) polymerase mRNA (The clone is 14 nt longer than the polymerase at 5' end; There is a point mutation at nt 159 of the clone)
GCCGCTCAGGCGCCTGCGGCTGGGTGAGCGCACGCGAGGCGGCGAG
GCGGCAGCGTGTTTCTAGGTCGTGGCGTCGGGCTTCCGGAGCTTTGC
CGGCAGCTAGGGGAGGATGGCGGAGTCTTCGGATAAGCTCTATCGAG
TCGAGTACGCCAAGAGCGGGCGCGCCTCTTGCAAGAAATGCAGCGAG
AGCATCCCCAAGGACTCGCTCCGGATGGCCATCATGGTGCAGTCGCC
CATGTTTGATGGAAAAGTCCCACACTGGTACCACTTCTCCTGCTTCTG
GAAGGTGGGCCACTCCATCCGGCACCCTGACGTTGAGGTGGATGGGT
TCTCTGAGCTTCGGTGGGATGATCAAGCAGAAAGTCAAGAAGACAGC
GGAAGCTGGAGGAGTNCAGG

SEQ ID 44
Pr3-119 Homo sapiens tankyrase, TRF-interacting ankyrin-related polymerase (TNKS) mRNA, and translated products (point mutation at nt 129 of the clone)
TAAAGGAAAGTATGAAATCTGCAAGCTCCTTTTAAAACATGGAGCAG
ATCCAACTAAAAAGAACAGAGATGGAAATACACCTTTGGATTTGGTAA
AGGAAGGAGACACAGATATTCAGGACTTACTGAGAGGGGATGCTGCT
TTGTTGGATGCTGCCAAGAAGGGCTGCCTGGCAAGAGTGCAGAAGCT
CTGTACCCCAGAGAATATCAACTGCAGAGACACCCAGGGCAGAAATT
CAACCCCTCTGCACCTGGCAGCAGGCTATAATAACCTGGAAGTAGCT
GAATATCTTCTAGAGCATGGAGCTGATGTTAATGCCCAGGACAAGGG
TGGTTTAATTCCTCTTCATAATGCGGCATCTTATGGGCATGTTGACA

SEQ ID 45
Pr3-128 Homo sapiens proteasome sub-unit HSPC mRNA
GAAGAAACAAAAGAAAGCATCATGATGAATAAAATGTCTTTGCTTGTA
ATTTTTAAATTCATATCAATCATGGATGAGTCTCGATGTGTAGGCCTT
TCCATTCCATTTATTCACACTGAGTGTCCTACAATAAACTTCCGTATTT
TTA

SEQ ID 46
Pr3-146 Human poly(ADP-ribose) polymerase mRNA (point mutation at nt 140 of the clone)
GCGATGNCTATTACTGCACTGGGGACGTCACTGCCTGGACCAAGTGT
ATGGTCAAGACACAGACACCCAACCGGAAGGAGTGGGTAACCCCAAA
GGAATTCCGAGAAATCTCTTACCTCAAGAAATTGAAGGTTAAAAAACA
GGACCGTATATTCCCCCCAGAAACCAGCGCCTCCGTGGCGGCCACGC
CTCCGCCCTCCACAGCCTCGGCTCCTGCTGCTGTGAACTCCTCTGCTT
CAGCAGATAAGCCATTATCCAACATGAAGATCCTGACTCTCGGGAAG
CTGTCCCGGAACAAGGATGAAGTGAAGGCCATGATTGAGAAACTCGG
GGGGAAGTTGACGGGGACGGCCAACAAGGCTTCCCTGTGCATAAGCA
CCAAAAAGGAGGTGGAAAAGATGAATAAGAAGATG

SEQ ID 47
Pr3-152 Homo sapiens ribosomal protein L10
AGAACANGGAGCATGTGATTGAGGCCCTGCGCAGGGCCAAGTTCAAG
TTTCCTGGCCGCCAGAAGATCCACATCTCAAAAAGTGGGGCTTCAAC
AAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCT
CATCCCAGATGGCTGTGGGGTCAAGTACATCCCCAGTCGTGGCCCTC
TGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGC
CCCCCTCTTAATACTCACCAATAAATTCTACTTCCTGTCCAAAAAAAA
AAA

SEQ ID 48
Pr3-154 Homo sapiens clone Xu-3 immunoglobulin heavy chain variable region mRNA
GTCGTGGACCTCCTGCACAAGAACATGAAACACCTGTGGTTCTTCCTC
CTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGTTACA
GCAGTGGGGCGCAGGACTCTTGAAGCCTTCGGAGACCCTGTCCCTCA
CCTGCGCNTGTCTATGGTGGGTCCTTAAGTGGTTATGGCTGGAGCNT
GGATCCGCCAGCCCCCAGGGAAGGGGCTTGGAGTGGATTGGGGAAG
TCGACCATCGTGGCAGCGCCAATTACCAGTCGGCCCTCCAGAGTCGA
GTCTCCGTATCATTGGACACGTCCAAGAACCAGGTCTCCCTGAGGCT
GAACTCAGTGACCGCCGCGGACACGGCTGTTTATNCTGTGCGAGAGG
CCTAATATAAAGCAATGGCTCTATTTGGGC

SEQ ID 49
Pr3-155 Homo sapiens phospholipase C, gamma 1 mRNA
GCCAGATCACGTGGAGCCGGGGCGCCGACAAGATCGAGGGGGCCAT
TGACATTCGTGAAATTAAGGAGATCCGCCCAGGGAAGACCTCACGGG
ACTTTGATCGCTATCAAGAGGACCCAGCTTTCCGGCCGGACCAGTCA
CATTGCTTTGTCATTCTCTATGGAATGGAATTTCGCCTGAAAACGCTG
AGCCTGCAAGCCACATCTGAGGATGAAGTGAACATGTGGATCAAGGG
CTTAACTTGGCTGATGGAGGATACATTGCAGGCACCCACACCCCTGC
AGATTGAGAGGTGGCTCCGGAAGCAGTTTTACTCAGTGGATCGGAAT
CGTGAGGATCGTATATCAGCCAAGGACCTGAAGAACATGCTGTCCCA
GGTCAACTACCGGGTCCCAACC

SEQ ID 50
Pr3-157 Homo sapiens ribosomal protein S10 mRNA
GTACCTTACCAATGAGGGTATCCAGTATCTCCGTGATTACCTTCATCT
GCCCCCGGAGATTGTGCCTGCCACCCTACGCCGTAGCCGTCCAGAGA
CTGGCAGGCCTCGGCCTAAAGGTCTGGAGGGTGAGCGACCTGCGAG
ACTCACAAGAGGGGAAGCTGACAGAGATACCTACAGACGGAGTGCTG
TGCCACCTGGTGCCGACAAGAAAGCCGAGGCTGGGGCTGGGTCAGC
AACCGAATTCCAGTTTAGAGGCGGATTTGGTCGTGGACGTGGTCAGC
CACCTCAGTAAAATTGGAGAGGATTCTTTTGCATTGAATAAACTTACA

GCCAAAAAAACCTTA

SEQ ID 51
Pr3-160 Homo sapiens poly(ADP-ribose) synthetase mRNA
AATCCGGGCACCAGGTTCGGTGCCCTCCTTCCCTGCGAGGAATGCTC
GGGTCAGCTGGTCTTCAAGAGCGATGCCTATTACTGCACTGGGGACG
TCACTGCCTGGACCAAGTGTATGGTCAAGACACAGACACCCAACCGG
AAGGAGTGGGTAACCCCAAAGGAATTCCTGAGAAATCTCTTACCTCA
AGAAATTGAAGGTTAAAAAAACAGGACCGTATATTCCCCCCAGAAACC
AGCGCCTCCGTGGCGGCCACGCCTCCGCCCTCCACAGCCTCGGCTCC
TGCTGCTGTGAACTCCTCTGCTTCAGCAGATAAGCCATTATCCAACAT
GAAGATCCTGACTCTCGGGAAGCTGTCCCGGAACAAGGATGAAGTGA
AGGCATGATTGAGAAACTCGGGGGGAAGTTGACGGGGA

SEQ ID 52
Pr3-163 Homo sapiens mitochondrial DNA (A point mutation at nt 169 of the clone)
AGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGTGTGAGGCGTATT
ATACCATAGCCGCCTAGTTTCAAGAGTACTGCGGCAAGTACTATTGAC
CCAGCGATGGGGGCTTCGACATGGGCTTTAGGGAGTCATAAGTGGAG
TCCGTAAAGAGGTATCTTTACTATAAAGGCTATTGTGTAAGCTAGTCA
TATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTGGGCAGTGAGAGT
GAGTAGTAGAATGTTTAGTGAGCCTAGGGTGTTGTGAGTGTAAATTA
AGTGCGATGAGTAGGGGAAGGGAGCCTACTAGGGTGTAGAATAGGA
AGTATGTCCTGCGTTCAGGCGTTCTGCTGGTTGCCTCATCGGGTGAT
GATAGCCAAGGTGGGGATAAGTGTGGTTCCAAAC

SEQ ID 53
Pr3-165 Homo sapiens ribosomal protein S8
GAGCGATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAAACC
GGGGGCAAGAGAAAGCCCTACCACAAGAAGCGGAAGTATGAGTTGG
GGCGCCCAGCTGCCAACACCAAGATTGGCCCCCGCCGCATCCACACA
GTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGA
CGTGGGGAATTTCTCCTGGGGCTCAGAGTGTTGTACTCGTAAAACAA
GGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTA
CCAAGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCG
TACCGACAGTGGTACGAGTCCCACTATGCGCTGCCCTGGGCCGCAAG
AAGGGAGCCAAGCTGACT

SEQ ID 54
Pr3-168 Homo sapiens ubiquitin specific protease 8 (USP) mRNA
GGCACATTGGCTAAAGGCTCTTTGGAGAATGTTTTGGATTCCAAAGA
CAAAACCCAAAAGAGCAATGGTGAAAAGAATGAAAAATGTGAGACCA
AAGAGAAAGGAGCAATCACAGCAAAGGAACTATACACAATGATGACG
GATAAAAACATCAGCTTGATTATAATGGATGCTCGAAGAATGCAGGA
TTATCAGGATTCCTGTATTTTACATTCTCTCAGTGTTCCTGAAGAAGC
CATCAGTCCAGGAGTCACTGCTAGTTGGATTGAAGCACACCTGCCAG
ATGATTCTAAAGACACATGGAAGAAGAGGGGGNAATGTGGAGTATTG
TGGGTACTTCTTGACTGGGTTTAAGTTCTGCCAAAGATTTACCAGATT
GGAACCAACTCTCCCGGAGTTTGAAAGATGCACTTTTCAGGGGGGAA
AGTAAAACTGGTCCTGCNCATGAGCCTTTGGNTTTAANGGGGGGTTT
GAAACTGGTCCTTTTTNTNCCCCGTTTCCACAAGCTTANGGGCNTCCC
CCNCACCCNANAAAANNGGGNTTCATNGGGTTTNCTTTCCCTTNGGAA
AAAAAATCTTTTAAACGGGGNCCACCCCCCCTTTTTAAAAN

SEQ ID 55

Pr3-170 Homo sapiens sgk protein kinase
TACCNTGTTTGNGCTCGCGCGCCTGCAGGTCGACACTAGTGGATCCA
AAG
CAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCG
TCAAGGAAGCTGCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCA
CGGACTCTTTCCTCTGAACCCTGTTAGGGCTTGGTTTTAAAGGATTTT
ATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGGTGGAGCCGCCAGC
TGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGCA
ATCTTATTGCACACTGTTCGCTGGAAGCTTTTTGAAGAGCACATTCTC
CTCAGTGAGCTCATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGG
TGCTATCTCTGAAACGAGCGTTAAGAGTGCCCGCCTTAGACGGAGCA
NGGAGTTTTCGTTAGAAAAGCGGACGCTGTTCTAAAAAANGTCTCTG
GCAGATCTGTCTGGGCTGGTGATGACNAATATTATGAAAATGTGNCC
TTTNTGAANAAAATGGGGTTAGCTTCNAACTTTCTTTCGCAAGGGTTC
AAGTTTTTATTTNCCTTGGGAATNCCTGGGGAACCCCCGGGGAAGGG
GGGATGCCNGANCAAAGGNTTTTGTTTAGCCNNAAGGGGACCTTGCG
GACTNCACGGGGAAATTTNTTTGTTT

SEQ ID 56
Pr3-174 Homo sapiens mitochondrial genome
GTCACCAAGACCCTACTTCTAACCTCCCTGTTCTTATGAATTCGAACA
GCATACCCCCGATTCCGCTACGACCAACTCATACACCTCCTATGAAAA
AACTTCCTACCACTCACCCTAGCATTACTTATATGATATGTCTCCATA
CCCATTACAATCTCCAGCATTCCCCCTCAAACCTAA

SEQ ID 57
Pr3-176 Homo sapiens metastasis associated 1 (MTA1) mRNA
GGGACATCTCCAGCACCCTCATCGCCCTGGCCGACAAGCACGCAACC
CTGTCAGTCTGCTATAAGGCCGGACCGGGGGCGGACAACGGCGAGG
AAGGGGAAATAGAAGAGGAAATGGAGAATCCGGAAATGGTGGACCT
GCCCGAGAAACTAAAGCACCAGCTGCGGCATCGGGAGCTGTTCCTCT
CCCGGCAGCTGGAGTCTCTGCCCGCCACGCACATCAGGGGCAAGTGC
AGCGTCACCCTGCTCAACGAGACCGAGTCGCTCAAGTCCTACCTGGA
GCGGGAGGATTTCTTCTTCTATTCTCTAGTCTACGACCCACAGCAGAA
GACCCTGCTGGCAGATAAAGGAGAGATTCGAGTAGGAAACCGGTACC
AGGCAGACATCACCGACTTGTTAAAAGAAGGCGAGGAGGATGGCCGA
GACCAGTCCAGGTTTGGAGACCCAAGTGTNGGGAGGGGCACAACCCA
CTTACAGACAAGCCAGATGNNCATTCTTGGGNGGNGGGCCGCTTTTG
GGGCACCTTCCACGGGNCCTGGACTGAGANNTTTCTTCCACACCCAC
TTGCAAAGANCNCCNAATTGCTTCCNAAAATANNCCTTTTCCNCCCCT
GGGTTCTTTCAAAANAAATTTACAAATTTCAGGC

SEQ ID 58
Pr3-179 Homo sapiens trans-Golgi p230 mRNA
CCGAGGCCAGCCAGTGGCACCCGGAAGAAAGAGACGCGGCGGCGGC
GACGCCGACACCCTCAGGACGAGTGTCCGGACTTGCCCACAGCCTCA
AGGAGGAGACGGCGAGGCCCGGCCCCCGCTGTCCCTGGTGTAAAGA
AGTCGCCGTAGCCGTCGCGGCCGGGACTCCCCGGGCTCTCGCCCTTC
AGGTTTCGTTGACACTCAGGACCGTACGTACGCTGCGCCATGTTCAA
GAAACTGAAGCAAAAGATCAGCGAGGAGCAGCAGCAGCTCCAGCAG
GCGCTGGCTCCTGCTAGGCGTCCTCCAATTCTTCAACACCAACAAGA
ATGAGGAGCAGGACATCTTCATTTACAGAGCAACTTGATGNAAGGTA
CACCCAATAGAAGAGTTCAAGGTGGACACACAAGTCTTTTGCACAGA
AAGCTTCAGTTCCNGGTGCCCTCGGGGGAGTCTTTGTTTTNGAAGTC
CGATAAGGAATTNTTTTCCGGNCTTTTTTAAAGAGTTTTTTGGTCCAA
AATNTTTCAAAAAATCCTGAATGATTGACTGGAAGNTCTGCCGTTTTG
ATCCCCCTTTTTTGATGNNGGGTAAAAATTGGGGGGGATTTNANACG

NTTAAAAAAAAATGTTTTCNGGTTGNAAAAAAGAANAANN

SEQ ID 59
Pr3-186 Homo sapiens Surf-5 and Surf-6 genes
AGAAAACACAAAAGAAATTCCGGAAGCGAGAAGAGAAGGCTGCTGAG
CACAAGGCCAAGTCCTTGGGGGAGAAATCTCCAGCAGCCTCTGGGGC
CAGGAGGCCTGAGGCAGCCAAAGAGGAAGCAGCTTGGGCTTCCAGCT
CAGCAGGGAACCCTGCAGATGGCCTGGCCACTGAGCCTGAGTCTGTC
TTTGCTCTGGATGTTCTGCGACAGCGACTGCATGAGAAGATCCAGGA
GGCCCGGGGCCAGGGCAGTGCCAAGGAGCTGTCCCCTGCCGCCTTG
GAGAAAAGGCGGCGGAGAAAGCAGGAACGGGACCGGAAGAAGAGGA
AGCGAAAGGAGCTGCGGGCGAAAGANAAGCCAGGAAGGCTGAGGAG
GCCACGGAGGCCCAGGAGGTGGTGGAGGCAACCCCAGAGGGGGCCT
GCACGGACCNCANGAGCCCCCGGCTTGTCTTCATTAGGGGGGAGGTG
AGCGAAACAACCGGCCACAAGGGGCACCAAAAAAAAAAAAAGCANAGG
TGAAGGGAACCTCNCCCTNCCGGAGAATACCGCANTTTTGAACCTGC
GCNCCGAAAACCGTTGANAANTCGCCCNATGGGGGAAGCCCNGACTG
GGCAAANA

SEQ ID 60
Pr3-197 Homo sapiens calcium binding protein (ALG-2) mRNA (6 nt deletion and a point mutation)
GGTCTCTCGTCGCTGCAGGCGCCTCAGCCCAGCCGCGTGCCTTGGCC
CATGGCCGCCTACTCTTACCGCCCCGGCCCTGGGGCCGGCCCTGGGC
CTGCTGCAGGCGCGGCGCTGCCGGACCAGAGCTTCCTGTGGAACGTT
TTCCAGAGGGTCGATAAAGACAGGAGTGGAGTGATATCAGACACCGA
GCTTCAGCAAGCTCTCTCCAACGGCACGTGGACTCCCTTTAATCCAGT
GACTGTCAGGTCGATCATATCCATGTTTGACCGTGAGAACAAGGCCG
GCGTGAACTTCAGCGAGTTCACGGGTGTGTGGAAGTACATCACGGAC
TGGCAGAACGTCTTCCGCACGTACGACCGGGACAACTCCGGGATGAT
CGATAAGAACGAGCTGAAGCAGGCCCTCTCAGGCTACCGGCTTNTNT
GACCAGTTCCACGACATCCTATTCGAAAAGTTTGACAGGCAGGGACG
GGGCAAAATCGCTTCAACACTTTATCANGGCTGNATTGTCTGAANAG
GTGGCGGTNTTTTAAACTTCACCCGGATAGGANGTGTTTAAGGGGTC
ACNAAAAANCTGCCANGNTTTAAAANTCGAAGACNGCCCCTTGGGAG
GGCCCCACTNGGAAGGCCAATGTNCCNT

SEQ ID 61
Pr3-200 Mus musculus BS4 peptide mRNA
GCGCAGGGATGGCACAAAAGAAATATCTTCAAGCAAAATTGACCCAG
TTTTTAAGGGAAGACAGGATTCAACTTTGGAAACCTCCATATACAGAT
GAAAATAAAAAAGTTGGTTTGGCATTAAAGGACCTTGCTAAGCAGTA
CTCTGACAGACTAGAATGCTGTGAAAATGAAGTAGAAAAGGTAATAG
AAGAAATACGTTGCAAGGCAATTGAGCGTGGAACAGGAAATGACAAT
TATAGAACAACGGGAATTGCTACAATCGAGGTGTTTTTACCACCAAGA
CTAAAAAAAGATAGGAAAAACTTGTTGGAGACCCGATTGCACATCAC
TGGCAGAGAACTGAGGTCCAAAATAGCTGAAACCTTTGGACTTCAAG
AAAATTATATCAAAATTGTCATAAATAAGAAGCAACTACACTAGGGAA
AACCCTTGAAGAAAAGGCGTGGCTCCAATGTGAAAGCGATGGTGCTT
GACTAAAACATCTGAAAGGACGCAGGAAACTTCCGTTGGGGAAGAGA
GCAAAANAGGCCACTCAAGAAAACANTCGNGNCAGANGGCTTGAATC
TGGCAGAAGCACNAAAGNGGGGGACCAAAGAACCCNCTTTAACTTNT
TACNGNCGGCNATN

SEQ ID 62

Pr3-203 Homo sapiens Pig11 (PIG11 mRNA)
GGCTCTGGCACACAGCTGTGCTCACAAAATACTGGGTGGCTTGGTTA
GAGCTAATTGTAGTGGAGCCTGCAGGTGAGGGTGAGGGAGGGGGCT
GCAGGTCAGGTAAGATCTGGAAGACAGACGTCAGCTTGGAGGGCAG
GGGGACTCTAAGGCAAGGAGATTTACAGTTGGGAAGGAGGCAGTGG
CAGAGGGGTGAGGGACAGGGGCCCTTAAGTCCAGCGAGGAAAGCTC
GGTGTGGGCCCGCTCTACGCTCCGTTTGGGGTGACCTGGAACGCCTC
TTCTCCCAGCTCCCTCCAGCCATCAGCAGCCTCTTGTCAAGCTTCTGC
CTCGCCCCAGTCTATCCCCAACCCCAAATCAAGACCACCTTTCTTCAC
GGTCACTATTTATTCTTTGGTCCTTTTCTTTTTGTAAGAAACATTCACA
AAAACCAGTGCCNNNCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNAAAAACTCGGGAGTCTTTTAAGGGGGCGNGGC
CNTNGNTTTCCCCGGGGGGGCCCGGNAAAGGNCCCCATNCCTTTNGG
GGGGGGGTTNNATNTGGGCCCGGNTTAAAACNTNGATNGNACCNCTG
GCT

SEQ ID 63
Pr3-206 Homo sapiens F1F0-type ATP synthase sub-unit d mRNA
GCAGCCAGGGTCGGTGAAGGATCCCAAAATGGCTGGGCGAAAACTTG
CTCTAAAAACCATTGACTGGGTAGCTTTTGCAGAGATCATACCCCAGA
ACCAAAAGGCCATTGCTAGTTCCCTGAAATCCTGGAATGAGACCCTC
ACCTCCAGGTTGGCTGCTTTACCTGAGAATCCACCAGCTATCGACTG
GGCTTACTACAAGGCCAATGTGGCCAAGGCTGGCTTGGTGGATGACT
TTGAGAAGAAGTTTAATGCGCTGAAGGTTCCCGTGCCAGAGGATAAA
TATACTGCCCAGGTGGATGCCGAAGAAAAAGAAGATGTGAAATCTTG
TGCTGAGTGGGGTGTCTCTCTCAAAGGCCAGGATTGTAGAATATGAA
GAAAGAGATGGAGAAGATGAAAGAACTTAATTNCTTTTGATCAGATG
ACCATTGANGGACTTGAATGAAGCTTTTCCAGAAACCAAATTAGACAA
GAAAAAGTNTCCTATTGGNCTCACCANCCATTGGGAATTATAAAATGA
GTCNGGAGGAAGTTTGGCCTTGNTACCATTTGGCCTTAAATATTATTT
TCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAAACCTCGGGGN
CTT

SEQ ID 64
Pr3-209 Homo sapiens ribosomal protein L18a
GCTGTCAAGCAGTTCCACGACTCCAAGATCAAGTTCCCGCTGCCCCA
CCGGGTCCTGCGCCGTCAGCACAAGCCACGCTTCACCACCAAGAGGC
CCAACACCTTCTTCTAGGTGCAGGGCCCTCGTCCGGGTGTGCCCCAA
ATAAACTCAGGAACGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAC

SEQ ID 65
Pr3-219 Human FACL5 for fatty acid coenzyme A ligase 5
GTTGCTGCTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAG
GACTCGCTGTGTCTGACAATGGGCCCTGCTTGGGATATAGAAAACCA
AACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGC
AGAGTACCTGGGTTCCTGTCTCTTGCATAAAGGTTATAAATCATCACC
AGACCAGTTTGTCGGCATCTTTGCTCAGAATAGGCCAGAGTGGATCA
TCTCCGAATTGGCTTGTTACACCGTACTCTATGGTAGCTTGTACCTCT
GTATGACACCTTGGGACCAGAAGCCATCGTACATATTGTCAACAAGG
CTGATATCGCCGTGGTGATCTGTGACACACCCCAAAAGGCATTGGTG
CTGATAGGGAATGTAAGAAGGCTCACCC

SEQ ID 66
Pr3-224 Homo sapiens DNA-binding protein (HRC1) mRNA (The clone contains alternative exon 1a; it might be a new isoform of HRC1)

CCGGATNGGGTCTCCAGGCTGGCGAGCGCCCAGGCCAGACTGGCCG
CTTTGTGCTTGTGCAGCGGCTTCGGGAGAAGGAGCGGCAGTTGCTGC
CACAAGAGTGTCCAGTGGGCGCCCAGGCCACCCTGCGGACAGTTTGC
CAGCGATGTCCAGTTTGTCCTGAGGCGCACAGGGCCCAGCCTAGCTG
GGAGGCCCTCCTCAGACAGCTGTCCACCCCCGGAACGCTGCCTAATT
CGTGCCAGCCTCCCTGTAAAGCCACGGGCTGCGCTGGGCTGTGAGCC
CCGCAAAACACTGACCCCCGAGCCAGCCCCCAGCCTCTCACGCCCTG
GGCCTGCGGCCCCTGTGACACCCACACCAGGCTGCTGCACAGACCTG
CGGGCCTGAACTCAGGGTGCAGAGGAC

CLAIMS

1. The use of an isolated nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 to detect or monitor cancer.

2. The use of a nucleic acid probe which is capable of hybridising under high stringency conditions to an isolated nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56,

SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 to detect or monitor cancer.

3. A method of detecting or monitoring cancer comprising the step of detecting or monitoring elevated levels of a nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 in a sample from a patient.

4. A method of detecting or monitoring cancer comprising the use of a nucleic acid molecule or probe according to claim 1 or claim 2 in combination with a reverse transcription polymerase chain reaction (RT-PCR).

5. A method of detecting or monitoring cancer comprising detecting or monitoring elevated levels of a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12,

SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66.

6. A method according to claim 5 comprising the use of an antibody selective for a protein or peptide as defined in claim 5 to detect the protein or peptide.

7. A method according to claim 7 comprising the use of an Enzyme-linked Immunosorbant Assay (ELISA).

18. Use or method according to any one of claims 1 to 7, wherein the cancer is prostate cancer is prostate cancer.

9. A kit for use with a method according to any one of claims 3-8 comprising a nucleic acid, protein or peptide, or an antibody as defined in any one of claims 3-8.

10. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5,

SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

11. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of a nucleic acid molecule hybridisable under high stringency conditions to a nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

12. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

13. A method of prophylaxis or treatment of cancer comprising the step of administering to a patient a pharmaceutically effective amount of an antibody capable of specifically binding a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40,

SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66.

14. A method according to any one of claims 10 to 11, wherein the cancer is prostate cancer.

15. A vaccine comprising a nucleic acid molecule having a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14,SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof and a pharmaceutically acceptable carrier.

16. A vaccine comprising a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID3, SEQ.ID4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11,

SEQ.ID.12, SEQ.ID.13, SEQ.ID.14,SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof, and a pharmaceutically acceptable carrier.

17. An isolated mammalian nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.43, SEQ.ID.44, SEQ.ID.52, SEQ.ID.60 and SEQ.ID.66 or a variant of a fragment thereof which encodes a prostate-associated antigen which is expressed in higher than normal concentrations in prostate cancer cells.

18. A vector comprising an isolated mammalian nucleic acid molecule according to claim 17.

19. A nucleic acid molecule comprising at least 15 nucleotides, the nucleic acid molecule being capable of hybridising to a molecule according to claim 17 under high stringency conditions.

20. An isolated protein or peptide comprising an amino acid sequence obtainable from a nucleic acid molecule according to claim 17, 18 or 19.

21. A nucleic acid probe capable of hybridising to a nucleic sequence as defined in SEQ ID 34, SEQ ID 35, SEQ ID 43, SEQ ID 44, SEQ ID 52, SEQ ID 60, SEQ ID 65 or SEQ ID 66, or a sequence complementary thereto, under high stringency conditions.

FIGURE 1

1. Esophageal cancer 2
2. Paired normal esophagus 2
3. Esophageal cancer 3
4. Paired normal esophagus 3
5. Esophageal cancer 4
6. Paired normal esophagus 4
7. Head and neck tumor 34
8. Paired normal head and neck 34